

FIGURE 1A

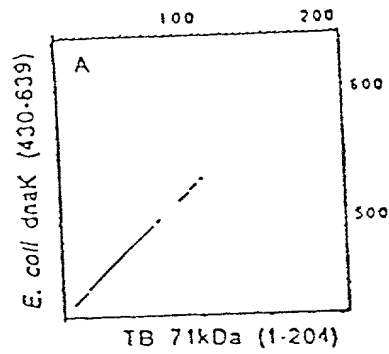
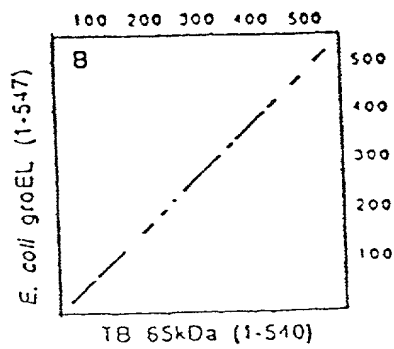


FIGURE 1B



	1	10	20	30	40	50	60	70
HUMP1	MLRLPTVFRQMRPVSRLAPHLTRAYAKDVKFGADARALMLQGVDLLADAVAVTMGPKGRTVIEEQSWGS							
GROEL	-----MA-----AKDVKFGNDARVKMLRGVNVVLADAVKVTLGPKGRNVVLDKSFGA							
	71	80	90	100	110	120	130	140
HUMP1	PKVTKDGVTVAKSIDLKDKYKNIGAKLVQDVANNTNEEZAGDGTATVLRSLIAKEGFEKISKGANPVEI							
GROEL	PTITKDGVSVAIEIEPEDKFENMGAQMVKEVASKANDAAGDGTATVLAQAIITEGLKAVAAGMNPMDL							
	141	150	160	170	180	190	200	210
HUMP1	RRGVMLAVDAVIAELKKQSKPVTTPEEIAQVATISANGDKEIGNIISDAMKKVGRKGVITVKDGKTLNDE							
GROEL	KRGIDKAVTAAVEELKALSVPSCSDSKAIAQVGTISANSDETGVKLIAMDKVGKEGVITVEDGTGLQDE							
	211	220	230	240	250	260	270	280
HUMP1	LEIIIEGMKFDRGYISPYFINTSKGQKCEFDAYVLLSEKKISSIQSIVPALEIANAHRKPLVITAEVDVG							
GROEL	LDVVEGMQFDRGYLSPYFINKPETGAVELESFFILLADKKISNIREMLPVLEAVAKAGKPLIIAEDVEG							
	281	290	300	310	320	330	340	350
HUMP1	EALSTLVNRLKVGLQVVAVKAPGFGDNRKNQLKDMAIATGGAVFGEGLTLNLEDVQPHDLGKVGEVIV							
GROEL	EALATAVVNTIRGIVKVAAVKAPGFGDRRKAMLQDIATLTGGTVISEE-IGMELEKATLEDLGQAKRVVI							
	351	360	370	380	390	400	410	420
HUMP1	TKDDAMLLKKGKGDKAQIEKRIQEIIEQLDVTTSSEYEKEKLNERLAKLSDGVAVLKVGGSVDVEVNEKKDF							
GROEL	NKDTTTIIDGVGEEAAIQGRVAQIROQIEEATSDYDREKLQERVAKLGGVAVIKVGAATEVEMKEKKAF							
	421	430	440	450	460	470	480	490
HUMP1	VTDALNATRAAVEEGIVLGGGCALLRCIPALDSLTPANEDQKIGIEIIKRTLKIPAMTIKNAGVEGSL							
GROEL	VEDALHATRAAVEEGVVAGGGVALIRVASKLADLRGQNEQNVVSSSL-RAMEAPLRQIVLNCGEEPSV							
	491	500	510	520	530	540	550	560
HUMP1	VEKIMQSSSEVGYDAMAGDFVNMVEKGIIDPTKVVRTALLDAAGVASLLTTAEVVVTEIPKEEKDPGGMG							
GROEL	ANTVKGGDGNYGYNAAATEEYGNMIDMGILDPTKVTRSALQYAASVAGLMITTECMVTDLPKND-AADLG							
	561	570						
HUMP1	MGGMGG--GMGGGMF							
GROEL	AGGMGGMGGMGGMM-							

Total score = 4667, 5 breaks
 276 identities out of 545 possible matches between residues

25 random runs
 Alignment score = 65.34 SD Standard deviation = 18.94 Mean = 3429.48

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      1      10      20      30      40      50      60      70
      ,      ,      ,      ,      ,      ,      ,      ,
HUMPI MLRLPTVFRQMRPVSRVLAPHLTRAYAKDVKFGADARALMLQGVDLLADAVAVTMGPKGRTVIEEQSWG
      :      :      :      :      :      :      :      :
ML65K M-----AKTIAYDEEARRGLERGLNSLADAVKVTLGPKGRNVVLEKKWGA

      71      80      90      100      110      120      130      140
      ,      ,      ,      ,      ,      ,      ,      ,
HUMPI PKVTKDGVTVAKSIDLKDKYKNIGAKLVQDVANNTNEEAGDGTATVLRSLAKEGFEKISKGANPVEI
      :      :      :      :      :      :      :      :
ML65K PTITNDGVSIAKEIELEDPEYKIGAEVLVKEVAKKTCDVAGDGTATVLAQALVKEGLRNVAAGANPLGL

      141      150      160      170      180      190      200      210
      ,      ,      ,      ,      ,      ,      ,      ,
HUMPI RRGVMLAVDAVIAELKKQSKPVTTPEEIAQVATISANGDKEIGNIISDAMKKVGRKGVITVKDGKTLNDE
      :      :      :      :      :      :      :      :
ML65K KRGIEKAVDKVTETLLKDAKEVETKEQIAATAAISA-GDQSIGDLIAEAMDKVGNEGVTVEESNTFGLQ

      211      220      230      240      250      260      270      280
      ,      ,      ,      ,      ,      ,      ,      ,
HUMPI LEIIIEGMKFDRGYISPYFINTSKGQKCEFDAYVLLSEKKISSIQSIVPALEIANAHRKPLVIAEDVDG
      :      :      :      :      :      :      :      :
ML65K LELTEGMRFDKGYISGYFVTDARQEAVLEEPYILLVSSKVVSTVKDLLPLEKVIQAGKSLIIAEDVEG

      281      290      300      310      320      330      340      350
      ,      ,      ,      ,      ,      ,      ,      ,
HUMPI EALSTLVNLRLKVGLQVAVKAPGFGDNRKNQLKDMAIATGGAVFGEEGLTLNLEDVQPHDLGKVGEVIV
      :      :      :      :      :      :      :      :
ML65K EALSTLVVNKIRGTFSKAVKAPGFGDRRKAMLQDMAILTGAQVISEE-VGLTLENTDLSLLGKARKVVM

      351      360      370      380      390      400      410      420
      ,      ,      ,      ,      ,      ,      ,      ,
HUMPI TKDDAMLLKGKGDKAQIEKRIQEIIEQLDVTTSEYEKEKLNERLAKLSDGVAVLKVGGTSDVEVNEKKDR
      :      :      :      :      :      :      :      :
ML65K TKDETTIVEGAGDTDAIAGRVAQIRTEIENSDDSDYDREKLQERLAKLAGGVAVIKAGAATEVELKERKHR

      421      430      440      450      460      470      480      490
      ,      ,      ,      ,      ,      ,      ,      ,
HUMPI VTDALNATRAAVEEGIVLGGGCALLRCIPALDSLTPANEDQKIGIEIIRKTLKIPAMTIKNAGVEGSLI
      :      :      :      :      :      :      :      :
ML65K IEDAVRNAKAAVEEGIVAGGGVTLLQAAPALDKLKTGDEAT-GANIVKVALEAPLKQIAFNSGMEPGV

      491      500      510      520      530      540      550      560
      ,      ,      ,      ,      ,      ,      ,      ,
HUMPI VEKIMQSSSEVGYDAMAGDFVNMVEKGIIDPTKVVRTALLDAAGVASLLTTAEVVVTEIPKEEKDPGMA
      :      :      :      :      :      :      :      :
ML65K AEKVRNLSVGHGLNAATGEYEDLLKAGVADPVKVTRSAALQNAASIAGLFTT-EAVVADKPEKTAAPASD

      561      570
      ,      ,
HUMPI MGGMGGGGMGGGMF
      :      :
ML65K TGGMGG-MD---F

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Total score = 4552, 7 breaks

255 identities out of 540 possible matches between residues

25 random runs

alignment score = 47.73 SD Standard deviation = 23.86 Mean = 3413.16

FIGURE 4

	1	10	20	30	40	50	60	70
HUMP1	MLRLPTVFRQMRPVSRLAPHLTRAYAKDVKFGADARALMLQGVDLLADAVAVTMGPKGRTVIEQSWGS							
TS65K	M-----AKTIAYDEEARRGLERGLNALADAVKVTGLGPKGRNVVLEKKWGA							
	71	80	90	100	110	120	130	140
HUMP1	PKVTKDGVTVAKSIDLKDKYKNIGAKLVQDVANNTNEEAGDGTATTATVLARSIAKEGFEKISKGANPVEI							
TS65K	PTITNDGVSLAKEIELEDPEYKIGAEVLKEVAKKTDVAGDGTATTATVLAQALRKEGLRNVAAAGANPLGI							
	141	150	160	170	180	190	200	210
HUMP1	RRGVMLAVDAVIAELKKQSKPVTTPEEIAQVATISANGDKEIGNIISDANKKVGRKGVITVXDGKTLNDI							
TS65K	KRGIEKAVEKVTETLLKGAKEVETKEQIAATAAISA-GDQSIGDLIAEAMDKVGNEGVITVEESNTFGLK							
	211	220	230	240	250	260	270	280
HUMP1	LEIIEGMKFDRGYISPYFINTSKGQKCEFDAYVLLSEKKISSIQSIVPALEIANAHKPLVIAEDVDI							
TS65K	LELTEGMRFDKGYISGYFVTDPERQEAVLEDPYILLVSSKVSTVKDLLPLEKVGIGAKPLLIIEEDVEI							
	281	290	300	310	320	330	340	350
HUMP1	EALSTLVNLRLKVLQVAVKAPGFGDNRKNQLKDMAIATGGAVFGEEGLTLNLEDVQPHDLGKVGEVI							
TS65K	EALSTLVVNKIRGTFSVAVKAPGFGDRRKAMLQDMAILTGGQVISEE-VGLTLENADLSLLGKARKVV							
	351	360	370	380	390	400	410	420
HUMP1	TKDDAMLLKKGDKAQIEKRIQEIEQLDVTTSSEYEKEKLNERLAKLSDGVAVLKVGGTSDVEVNEKXD							
TS65K	TKDETTIVEGAGDTDAIAGRVAQIRQEIENSDDYDREKLQERLAKLAGGVAVIKAGAATEVELKERKH							
	421	430	440	450	460	470	480	490
HUMP1	VTDALNATRAAVEEGIVLGGGCALLRCIPALDSLTPANEDQKIGIEIIEKRTLKIPAMTIKNAAGVEGSI							
TS65K	IEDAVRNAKAAVEEGIVAGGGVTLLQAAPTLDLKL-LEGDEATGANIVKVALEAPLKQIAFNNSGLEPGI							
	491	500	510	520	530	540	550	560
HUMP1	VEKIMQSSSEVGYDAMAGDFVNMVEKGIIDPTKVVRTALLDAAGVASLLTTAEVVVTEIPKEEKDPGM							
TS65K	AEKVRNLPAGHGLNAQTGVYEDLLAAGVADPVKVTSAALQNAASIAGLFLTTEAVVADKPEKEKASVP							
	561	570						
HUMP1	MGGMGGGMGGGMF							
TS65K	----GGDMGGGMDF							

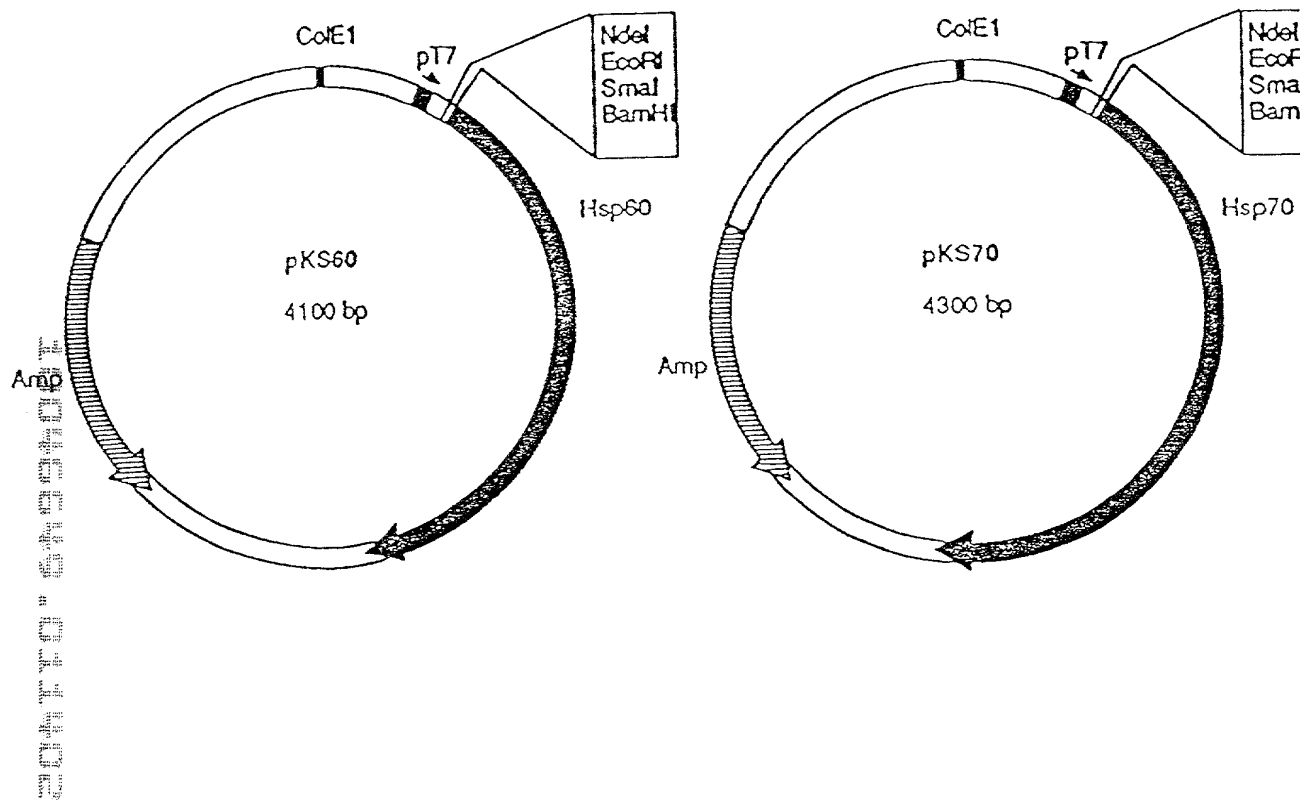
Total score = 4560, 5 breaks

257 identities out of 540 possible matches between residues

25 random runs

Alignment score = 49.36 SD Standard deviation = 23.23 Mean = 3413.15

Figure 5



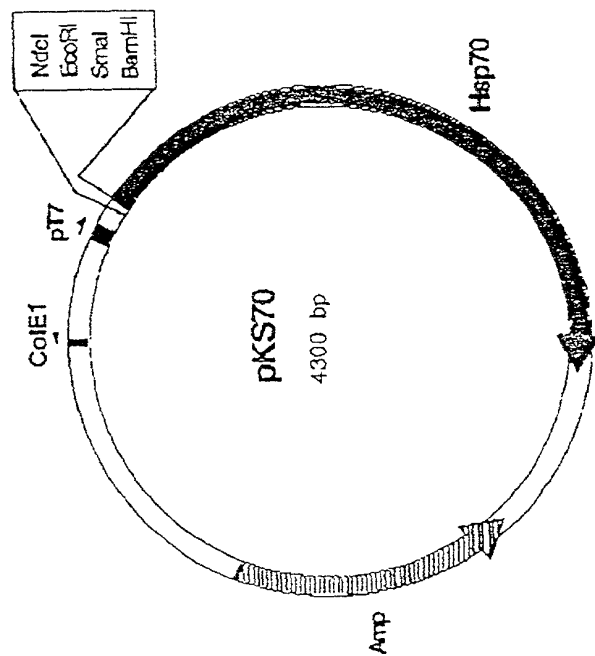
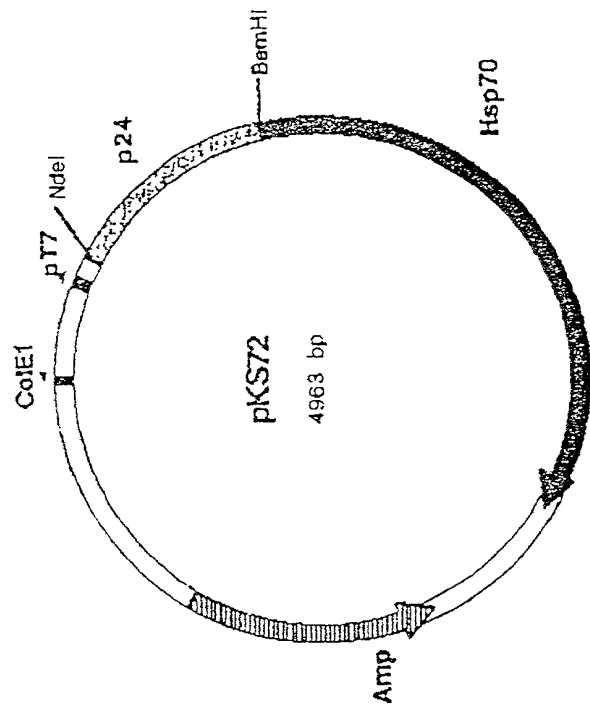


FIGURE 6

anti-p24 antibody titer
(3 weeks after boost)

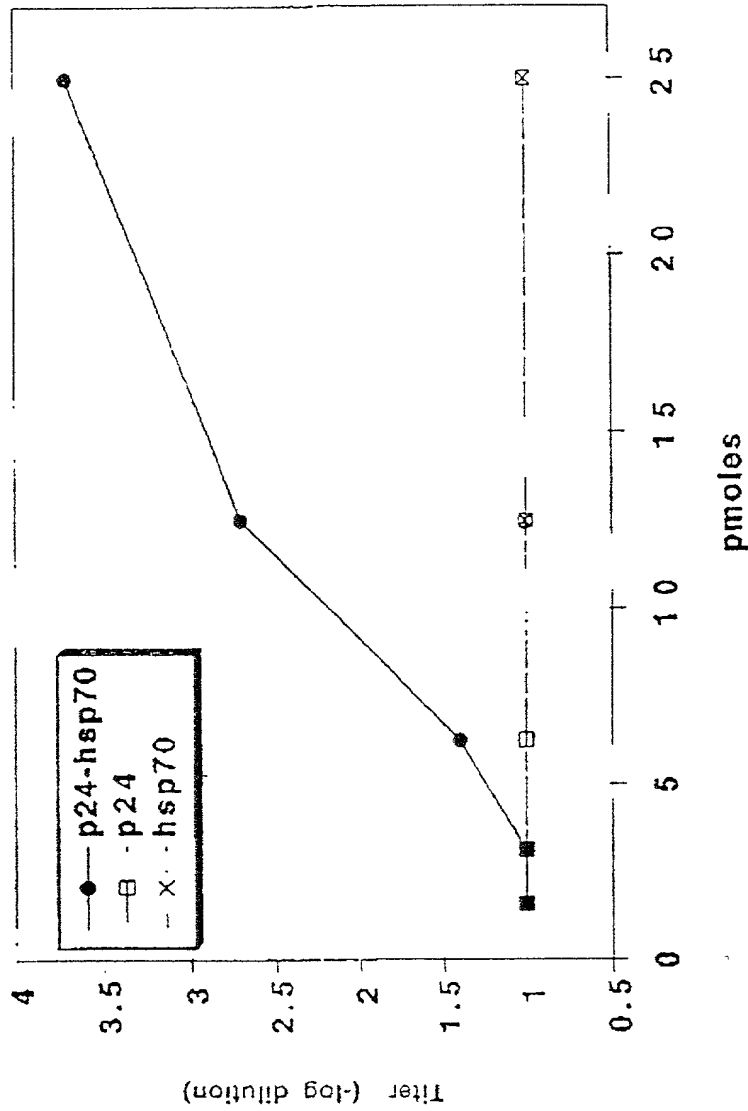


FIGURE 7